

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2000, 06:23:06 ; Search time 23795.2 seconds  
(without alignments)  
972.809 Million cell updates/sec

Title: US-09-227-881-1

Perfect score: 5300  
Sequence: 1 atcttgctcagttaccctc.....cagcacctctcagcacagc 5300

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues

Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*

1: gb\_da1:\*

2: gb\_da2:\*

3: gb\_om:\*

4: gb\_ov:\*

5: gb\_pac:\*

6: gb\_ph:\*

7: gb\_p11:\*

8: gb\_p12:\*

9: gb\_p1:\*

10: gb\_p12:\*

11: gb\_p13:\*

12: gb\_ro:\*

13: gb\_sy:\*

14: gb\_un:\*

15: em\_fun:\*

16: em\_hum1:\*

17: em\_hum2:\*

18: em\_in:\*

19: em\_om:\*

20: em\_or:\*

21: em\_ov:\*

22: em\_pac:\*

23: em\_ph:\*

24: em\_p1:\*

25: em\_ro:\*

26: em\_sy:\*

27: em\_un:\*

28: em\_hum1:\*

29: em\_hum2:\*

30: em\_in:\*

31: gb\_da3:\*

32: gb\_in1:\*

33: gb\_in2:\*

34: gb\_in3:\*

35: gb\_p14:\*

36: em\_ba1:\*

37: em\_ba2:\*

38: em\_htg1:\*

39: em\_htg2:\*

40: em\_htg3:\*

41: em\_htg4:\*

42: em\_htg5:\*

43: em\_htg6:\*

44: em\_htg7:\*

45: em\_htg8:\*

46: em\_htg9:\*

47: em\_htg10:\*

48: em\_htg11:\*

49: em\_htg12:\*

50: em\_htg13:\*

51: em\_htg14:\*

52: em\_htg15:\*

53: em\_htg16:\*

54: em\_htg17:\*

55: em\_htg18:\*

56: em\_htg19:\*

57: em\_htg20:\*

58: em\_htg21:\*

59: em\_htg22:\*

60: em\_htg23:\*

61: em\_hum3:\*

62: em\_hum4:\*

63: em\_hum5:\*

64: em\_hum6:\*

65: gb\_p15:\*

66: gb\_p16:\*

67: gb\_p17:\*

68: gb\_p18:\*

69: gb\_p19:\*

70: gb\_p20:\*

71: gb\_p21:\*

72: gb\_p22:\*

73: gb\_p23:\*

74: gb\_p24:\*

75: gb\_p25:\*

76: gb\_p26:\*

77: gb\_p27:\*

78: gb\_p28:\*

79: gb\_p29:\*

80: gb\_p30:\*

81: gb\_p31:\*

82: gb\_p32:\*

83: gb\_p33:\*

84: gb\_p34:\*

85: gb\_p35:\*

86: gb\_p36:\*

87: gb\_p37:\*

88: gb\_p38:\*

89: gb\_p39:\*

90: gb\_p40:\*

91: gb\_p41:\*

92: gb\_p42:\*

93: gb\_p43:\*

94: gb\_p44:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	5286	99.7	79376	65	HS454G6
C 2	5275.4	99.5	5300	11	AF007562
C 3	5235	98.8	170425	77	AC024490
C 4	1858	35.1	2800	66	HSKXOC1
C 5	423.4	8.0	1086	66	HSGLC1N1
C 6	423.4	8.0	1228	9	AB006686S1
C 7	189.8	3.6	161577	10	AC007688
C 8	189.8	3.6	193123	77	AC023790
C 9	189	3.6	199722	71	AC012404
C 10	187.8	3.5	97037	9	AC004973
C 11	187.8	3.5	135038	67	HDMRWXD703
C 12	185.8	3.5	76727	65	HS821D11

c	13	185.8	3.5	152044	79	AC026395
c	14	185.8	3.5	152097	78	AC025947
c	15	185.8	3.5	161499	72	AC015488
c	16	185.8	3.5	184656	86	AL161726
c	17	185.8	3.5	200681	69	AC008755
c	18	185.6	3.5	201372	86	AL157941
c	19	184.8	3.5	146190	89	AP001813
c	20	184.8	3.5	163494	89	AP002291
c	21	184.8	3.5	183341	89	AP001354
c	22	184.8	3.5	176029	11	AC011362
c	23	184.2	3.5	130020	67	HUAC004525
c	24	184	3.5	157304	78	AC024720
c	25	184	3.5	187709	73	AC016168
c	26	184	3.5	233734	70	AC011407
c	27	183.6	3.5	62070	88	AL358852
c	28	183.6	3.5	129370	89	AP000609
c	29	183.6	3.5	169333	89	AP002789
c	30	183.6	3.5	193171	74	AC018723
c	31	183.4	3.5	41407	11	AC053467
c	32	183.4	3.5	149138	79	AC026936
c	33	183.4	3.5	156331	90	HS193M11
c	34	183.4	3.5	174974	87	AL356055
c	35	183.4	3.5	193364	65	HS431A14
c	36	183.4	3.5	198583	74	AC019114
c	37	183.4	3.5	41936	35	CH19R30879
c	38	183.2	3.5	70128	10	AC007536
c	39	183.2	3.5	119483	9	AC005588
c	40	183.2	3.5	145528	9	AC003665
c	41	183.2	3.5	167943	65	HS267820
c	42	183.2	3.5	170245	65	HS109F14
c	43	183	3.5	42686	9	AC000093
c	44	183	3.5	91767	10	AC007748
c	45	183	3.5	112748	10	AC007242

## ALIGNMENTS

RESULT 1  
LOCUS HS4546/c  
DEFINITION Human DNA sequence from PAC 45466 on chromosome 1q24. Contains triallelic marker with inducible glucocorticoid response protein, TIGR, myocillin, ESTs and STS.

ACCESSION 298750  
VERSION 1  
KEYWORDS 1q24; myocillin; TIGR.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 79376)  
Deadman, R.  
Direct Submission  
(http://www.sanger.ac.uk/HGP/Chr1/) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humuery@sanger.ac.uk  
On Feb 14, 1998 this sequence version replaced gi:246060.  
IMPORTANT: This sequence is not the entire insert of clone 45466. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

## COMMENT

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with only a small overlap as described above.  
This sequence was generated from part of bacterial clone configs of human chromosome 1, constructed by the Sanger Centre chromosome 1 mapping group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr1/>

## FEATURES

## SOURCE

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.  
The true left end of clone 45466 is at 1 in this sequence. The true left end of clone 56089 is at 79273.  
45466 is from the library RPI3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong.  
For further details see <http://bacpac.med.buffalo.edu/>.

## repeat\_region

## prim\_transcript

/note="19 copies of 2 mer 82 & conserved"  
1914. >3968

/note="match: multiple ESTs  
match: R3676 AA043968 W63639 F12081 AA046699  
match: F02925 AA131540 W00634 R36066  
match: AA163561 F02925 AA131540 W00634 R36066  
match: AA13383 AA163561 N89173 AA174814 AA057059  
match: AA329084 W47082 AA043955 AA141783 AA353661  
match: AA046487 AA369741 H08313 AA186895 H32730  
match: H08333 H08236 M42052 D61944 R21102 N32353  
match: N30491 AA307150 AA192"

/note="22 copies of 2 mer 89 & conserved"  
4051. 4183

/note="AluSg repeat: matches 1. 133 of consensus  
incomplete repeat"  
4200. 4502

/note="AluSg repeat: matches 2. 301 of consensus"  
4659. 4851

/note="AluSx repeat: matches 2. 194 of consensus  
incomplete repeat"  
5216. 5345

/note="Alu repeat: matches 132. 1 of consensus  
incomplete repeat"  
7759. 7907

/note="MIR repeat: matches 174. 1 of consensus"  
7933. 9328

/note="TRIGER1 repeat: matches 1. 1472 of consensus"  
9332. 9626

/note="AluSg repeat: matches 1. 289 of consensus"  
9639. 10335

/note="TRIGER1 repeat: matches 1469. 2174 of consensus"  
10343. 10642

/note="AluSg repeat: matches 1. 300 of consensus"  
10643. 10856

/note="TRIGER1 repeat: matches 2175. 2417 of consensus"  
<10903. >16855

/note="endogenous retroviral sequence"  
10949. 11384

/note="LTR2 repeat: matches 31. 449 of consensus"  
15835. 15870

/note="18 copies of 2 mer 83 & conserved"  
16856. 17286

/note="LTR2 repeat: matches 31. 449 of consensus"  
17287. 17574

/note="AluSg repeat: matches 15. 300 of consensus"  
18294. 18650

/note="THE1B repeat: matches 358. 1 of consensus"  
18877. 19180

/note="Alu repeat: matches 301. 2 of consensus"  
19767. 20013

/note="MUT2 internal repeat: matches 5002. 4750 of  
consensus"

repeat\_region

repeat\_region

repeat\_region

repeat\_region

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repeat\_region

repeat\_region

repeat\_region

repeat\_region

repeat_region	20051..20118	/note="MUT1 repeat: matches 539..471 of consensus"
repeat_region	20130..20261	/note="AluB repeat: matches 131..1 of consensus incomplete repeat"
repeat_region	20264..20722	/note="MUT1 repeat: matches 482..1 of consensus"
repeat_region	20858..21223	/note="MST repeat: matches 394..1 of consensus"
repeat_region	21216..21302	/note="MUT2_internal repeat: matches 4520..4433 of consensus"
repeat_region	21403..21703	/note="MUT2_internal repeat: matches 3887..3580 of consensus"
repeat_region	21978..22337	/note="MUT2_internal repeat: matches 3218..2839 of consensus"
repeat_region	22363..22524	/note="MUT2_internal repeat: matches 2495..2317 of consensus"
repeat_region	22531..22839	/note="AluX repeat: matches 302..1 of consensus"
repeat_region	23007..23309	/note="AluSD repeat: matches 3..301 of consensus"
misc_feature	23286..>23580	/note="STS G07544"
misc_feature	23580..>23680	/note="STS G07436"
misc_feature	24008..24290	/note="AluB repeat: matches 298..6 of consensus"
repeat_region	23895..26364	/note="L1R2 repeat: matches 2..449 of consensus"
repeat_region	26397..26697	/note="AluSG repeat: matches 1..302 of consensus"
repeat_region	26719..27021	/note="AluX repeat: matches 1..302 of consensus"
repeat_region	29037..29334	/note="AluX repeat: matches 300..3 of consensus"
repeat_region	30028..30310	/note="AluX repeat: matches 1..301 of consensus"
repeat_region	30402..30559	/note="MUT2 repeat: matches 264..404 of consensus"
repeat_region	30402..30615	/note="MUT2A repeat: matches 264..453 of consensus"
prim_transcript	<30801..>31136	/note="match: 5' EST AA256902 clone 682136"
repeat_region	30980..31222	/note="MIR4B repeat: matches 199..431 of consensus"
repeat_region	31232..31558	/note="AluSC repeat: matches 299..1 of consensus"
repeat_region	31530..31654	/note="MIR4B repeat: matches 417..540 of consensus"
repeat_region	31836..32135	/note="AluY repeat: matches 300..1 of consensus"
repeat_region	32200..32301	/note="AluB repeat: matches 186..287 of consensus incomplete repeat"
repeat_region	32365..32483	/note="MIR repeat: matches 206..67 of consensus"
repeat_region	33283..33399	/note="MIR repeat: matches 77..196 of consensus"
repeat_region	33408..33667	/note="AluY repeat: matches 1..291 of consensus"
repeat_region	33956..34043	/note="MIR repeat: matches 80..167 of consensus"
repeat_region	34725..34904	/note="AluB repeat: matches 299..127 of consensus incomplete repeat"
repeat_region	34907..35207	/note="AluY repeat: matches 300..1 of consensus"
repeat_region	35212..35344	/note="AluB repeat: matches 133..1 of consensus"

	repeat_Lregion	incomplete repeat"
Oy	36545..35842	/note="AluJo repeat: matches 299. .1 of consensus"
Dd	68406 ATCTTTGTCAGTTACTCCTCAGGGCTATTGAATGAATAACAGATTAACAATGTGAAG	38190..38379 /note="MER3 repeat: matches 209. .13 of consensus"
Oy	61 tccataaacgtataagcctccaatcggaatgatttgccttcggcaggatgataagaacaa	38382..38682 /note="AluSx repeat: matches 1. .302 of consensus"
Dd	68346 TCCATAAACCGTAAAGCCTCCATTCGGATGTATGCTCTTGCGACGAGATPAAGAATCA	38836..38968 /note="MIR2 repeat: matches 145. .2 of consensus"
Oy	121 ggaagaagagatatccacgttagccaagtgcaccaagcgtgtctgcctctaattagta	38983..39279 /note="AluJb repeat: matches 3. .296 of consensus"
Dd	68286 GGAAGAAGAGATATCACAGTTAGCCAATGTCCAGGCCTGTGTCTCTTTATTAGTGA	39418..39773 /note="THE1A repeat: matches 354. .2 of consensus"
Oy	181 cagatgttgtcctctgacagaagacttatcttcaggaanaacacacatccaatatgytaa	39775..40120 /note="THE1B-INTERNAL repeat: matches 1580. .1234 of consensus"
Dd	68226 CAGATGTGTCCTCCTCAGAGAAGCATTTCTTCAGGAACATCATCAATATGTGAATTC	40757..41023 /note="AluJo repeat: matches 37. .301 of consensus"
Oy	241 catcaacaagaagcttaagaacaaggaatgagatgagcattggcccaggaaaatgtcac	41307..41589 incomplete repeat"
Dd	68166 CATCAAACGAGCGCTPAAACAAACAGAAAGAATGTGGCCTTGCCCAAGAAAAGCCAG	41307..41589 /note="Alusq repeat: matches 21. .303 of consensus"
Oy	301 gagagcaaaataatgtlgaaaaaataaacctttcccttctttttaatttcaggaaaaa	
Dd	68106 GAGAGCAATAATATGTAGAAAAATAAATTAACCTTTTCCCTTTTATTATTTTCAGAAAAATG	
Oy	361 atgagaccaaaatacaatgaaataagaaacaagctcagaaaaaaagatgtttccaaatg	
Dd	68046 ATGAGACCAAAATCAATGAATTAAGAAACAGCTCACAATAAAGATGTTCCAATTGG	
Oy	421 taattaaglatattgtctctcgtggagaagacctcaatgtgaccttgatvggaaaatggaa	
Dd	67986 TAATTAATATATTGTTCTTGTGGAGAACACTCCATGTGACCTTGATGTGAAAATGGAA	
Oy	481 aaagctcaaaagcatgatcgtatcagatccccaaaatlgatattatattttaaanaacag	
Dd	67926 AAACGCTCAAAAACATGATCTGTATCAGATCCCAAAATGGATTAATTATTTTTAAACCAAT	
Oy	541 ggcacacactctggygaagcagaatcagaagaagtcagtcagcaaaagcatacacatcac	
Dd	67866 GGCAATCACTCTGTGGGAGGCAAGTTACGAAGTCACTGTTAGCAAAAGGACATTAACAATAC	
Oy	601 agcaaatccaataatccgcaaatgcaggaggaataatgggagctgggaaaagcttccatac	
Dd	67806 AGCAAAATCAAAATATCCCAAAATCGAGAGAGAAATCGGAGCTGGAAAGCTTTCATATAC	
Oy	661 agtgatggcaggttgacacatgtctgcacaacacctcccgcttataaccaggaagcaaaa	
Dd	67746 AATGATATGGCGATGTGACCAATGTTGCCAACACCTCCCGTCTATACAGGGAACCAAAH	

OY 721 attgactgggtctaaagcctggaacttccaaaggaaatactgaaaaaactgagagcaaaacaaa 780  
|||||  
Db 67686 attgactgggcttaagccttgactcttaagggaaatctgaaaaactgagcaaaacaaa 67627  
OY 781 gacatggtttaaaaggcaacacagaacaatgtagaccttcaaaagcagctgccccctcaga 840  
|||||  
Db 67626 gacatggtttaaaaggcaacacagaacatgtgagaccttcaaaagcagcagccccctcaga 67567  
OY 841 gggagccctgaagcatttgcctttagaagaagccagcttctttaaagaaattcttaagaacac 900  
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Db 67566 gggagccctgaagcatttgcctttagaagaagccagcttctttaaagaaattcttaagaacac 67507  
OY 901 ttgaaagacatgaatcttcaaccattttaaagtaaaacaataatctgcaatgcaatcag 960  
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Db 67506 ttgaaagacatgaatcttcaaccattttaaagtaaaacaataatctgcaatgcaatcag 67447  
OY 961 tttagacatggtgcccaatttctaaagtcaggcatataagaatgctgtccagctcc 1020  
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Db 67446 tttagacatggtgcccaatttctaaagtcaggcatataagaatgctgtccagctcc 67387  
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Db 67386 ggaataggtcaagaatcatatagaatactgtgtcccatccttaacttctcagaatgac 67327  
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Db 66906 agcctctcaaatgtctgtagaatacagagcatgagtcacgcgcgcgcgcgcgcgcgcgcgc 66847  
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OY 1801 ttccatttgggcaatctgtgtgtgtatagggaggagagcattaccacagagatcct 1860  
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OY 1921 tgggtgtcttgaacacacgagccgctgcaacggtgtgtgtgttcttaactctctag 1980  
|||||  
Db 66486 tgggtgtcttgaacacacgagccgctgcaacggtgtgtgtgttcttaactctctag 66427  
OY 1981 gacctgtgtcttcaattctgt 2040  
|||||  
Db 66426 gacctgt 66367  
OY 2041 tatgagtaactatatactgagagacacacagagaaataatgtagaagagctacagc 2100  
|||||  
Db 66366 tatgagtaactatatactgagagacacacagagaaataatgtagaagagctacagc 66307  
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|||||  
Db 66306 cctacactcgtgtaggtgtagcaatctctcatgtagaagcgtgtagaagaaataatagca 66247  
OY 2161 gccaacttaaacccagctgtagaagaaagaaataaacacactttagaagatgtgcgc 2220  
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Db 66246 gccaacttaaacccagctgtagaagaaagaaataaacacactttagaagatgtgcgc 66187  
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Db 66186 agcatcccttaacagagcactctcctagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 66127  
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|||||  
Db 66066 gctcgtctccggtgaatcgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 66007  
OY 2401 ccaagaaagaaatgtagagagagaaatagctcaagagaaatctgtagagagagctgttc 2460  
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OY 2461 ctcaagagagaaaggggctccacgctcagagaaatctcagagaggtgtagagagagag 2520  
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Db 65946 ctcaagagagaaaggggctccacgctcagagaaatctcagagaggtgtagagagagag 65887  
OY 2521 tgggagagcgtgtagcgtgtagcgtgtagcgtgtagcgtgtagcgtgtagcgtgtagcgt 2580  
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OY 2581 gctgccaagatgtagaggt 2640  
|||||  
Db 65826 gctgccaagatgtagaggt 65767  
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ACCESSION AF007562  
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REFERENCE 1 (bases 1 to 5300)  
AUTHORS Nguyen,T.D., Chen,P., Huang,W.D., Chen,H., Johnson,D. and Polansky,J.R.  
TITLE Gene structure and properties of TIGR, an olfactomedin-related glycoprotein cloned from glucocorticoid-induced trabecular meshwork cells  
JOURNAL J. Biol. Chem. 273 (11), 6341-6350 (1998)  
MEDLINE 98165818  
REFERENCE 2 (bases 1 to 5300)  
AUTHORS Nguyen,T.D., Chen,P., Chen,H. and Polansky,J.R.  
TITLE Direct Submission  
JOURNAL Submitted (10-JUN-1997) Ophthalmology, University of California San Francisco, 10 Kirtham Street, San Francisco, CA 94143-0730, USA  
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ORIGIN

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Matches 5298; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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REFERENCE  
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TITLE  
JOURNAL  
COMMENT

2 (bases 1 to 170425)  
 Blatter, B., Baldwin, J., Barne, N., Bede, F., Boguslavsky, L.,  
 Anderson, S., Landers, J., Lander, E., Abraham, H., Allen, N.,  
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 Travers, M., Triglilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B.,  
 Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and  
 Zody, M.  
 Direct Submission  
 Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On May 25, 2000 this sequence version replaced g1:7249345.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 ----- Project Information  
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 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 28 contigs. The true order of the pieces  
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 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
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ACCESSION	2917171			
VERSION	2917171.1	GI:2425156		
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SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 1086)			

AUTHORS					Stone, E.M., Fingeret, J.H., Alward, W.L., Nguyen, T.D., Polansky, J.R., Sundén, S.L., Nishimura, D., Clark, A.E.F., Nysuen, A., Nichols, B.E., Riech, R., Kalenak, U.W., Craven, E.R. and Sheffield, V.C.
TITLE	JOURNAL	MEDLINE REFERENCE	AUTHORS		Identification of a gene that causes primary open angle glaucoma Science 275 (5300), 668-670 (1997)
REFERENCE	2 (bases 1 to 1086) Adem, M.F., Balmondun, A., Binisti, P., Brezin, A.P., Valiot, F., Becheviller, A., Descotte, J.C., Copin, B., Gomez, L., Chavente, A., Bach, J.F. and Garçon, H.J. Recurrent mutations in a single exon encoding the evolutionarily conserved opifacomedin-homology domain of TIGR in familial open-angle glaucoma Hum. Mol. Genet. 6 (12), 2091-2097 (1997)				
TITLE	JOURNAL MEDLINE REFERENCE AUTHORS	3 (bases 1 to 1086) Garçon, H.J. Direct Submission Submitted (20-JUN-1997) Garçon H.-J., Hopital Necker, INSERM U25, 161 rue de Sevres 75743 Paris cedex 15 FRANCE			
FEATURES	SOURCE	Location/Qualifiers			
	1..1086 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="1" /map="q23-q25" /feature_type="white blood cells"				
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BASE COUNT	277 a 282 c 316 g 211 t				
ORIGIN					
Query Match	Best Local Similarity 99.8% Pred. No. 9.6e-81; Matches 424; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
Oy	4876 agccatagggcctcggaacggtgcaggtttcataagtgcattgccagaagtgaatgaaatatca 4935				
Dd	I AGCATAGTGCGTCGCCACAGTAGCAAGTTTCATTGACTGACAGAGTGAAATGAAAATATA 60				
Oy	4936 actagaatatcatccttgtagaatccaagcacaccagtagtacctggtctaagtgtgatc 4995				
Dd	61 ACTAGAATATATATCTCTTGTGAATCACAGACACCAGTAGTCTCTGTATAGTGCTGTAC 120				

Oy		4996	gtctgctgcgtcgtcgatggacagccagggaataagaacttcatttg	5055
Dd		121	GTGCTGTGTCGTCTGTCTGTCTGTCTGTCTAACAACAGCGTGGATTTAGAACAATTATTTG	180
Oy		5056	ggcataggcatcaaatcttggagtcttccttttaaaagaacctccaacagactcttgtg	5115
Dd		181	GCGATATGGGTCATAAAATTGGCATGTCTTTTAATAAAAAGAACITCCAAACAGACTTTGTGG	240
Oy		5116	aagtttatctttaagaacctctgcgcgcgatgtagaaggcaaacccccctgtgccagacc	5175
Dd		241	AAGGTATTTTTCTTAGAATCTTCTGTGCAGCCTGAAGCAACCCTCTGTGCACAGCCCC	300
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Dd		301	ACCAAGCCTCACAGNGGCCACCTGTGCTCTCCCCTCAAAGAAGGCTGTGGCTCCCA	360
Oy		5236	ttaaaccctcttgtagctcgtggagctggcagcaagaaggccaccatccaggaccctc	5295
Dd		361	TAAACCTCTCTGTGAGCTCGGGCATGTAGCCACCAAGGCCACCATTCAGACCACTT	420
Oy		5296	acaagc 5300 	
Dd		421	ACAGC 425	
RESULT		6		
AB006686S1	LOCUS	AB006686S1	1228 bp DNA PRI	14-APR-2000
DEFINITION	Homo sapiens gene for myocillin, exon 1, complete sequence.			
ACCESSION	AB006686			
VERSION	AB006686.1 GI:2828342			
KEYWORDS	myocillin.			
SEGMENT SOURCE	1 of 3 Homo sapiens pre-pro-B cell cell_line:FLEB14-14 DNA, clone_1lb:BAC clone:X8780C12.  Homo sapiens Enkayojota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
ORGANISM REFERENCE AUTHORS TITLE	Escribanou,J., Ortego,J. and Coca-Prados,M. Isolation and characterization of cell-specific cDNA clones from a subtractive library of the ocular ciliary body of a single normal human donor: transcription and synthesis of plasma proteins J Biochem. 118 (5), 921-931 (1995)			
JOURNAL MEDLINE REFERENCE AUTHORS	96318503 2 (sites) Stone,E.M., Fingert,J.H., Alward,W.L., Nguyen,T.D., Polansky,J.R., Sundén,S.L., Nishimura,D., Clark,A.F., Nyström,A., Nichols,B.E., Ritch,R., Kalenak,J.W., Craven,E.R. and Sheffield,V.C. Identification of a gene that causes primary open angle glaucoma Science 275 (5300), 668-670 (1997)			
JOURNAL MEDLINE REFERENCE	97158493 3 (sites) Kudoba,R., Noda,S., Wang,Y., Minoshima,S., Asakawa,S., Kudoh,J., Mashima,Y., Oguchi,Y. and Shimizu,N. A novel myosin-like protein (myocilin) expressed in the connecting cilium of the photoreceptor: molecular cloning, tissue expression, and chromosomal mapping Genomics 41 (3), 360-369 (1997)			
JOURNAL MEDLINE REFERENCE	97312692 4 (sites) Kudoba,R., Kudoh,J., Mashima,Y., Asakawa,S., Minoshima,S., Hitojancik,J.F., Oguchi,Y. and Shimizu,N. Genomic organization of the human MYOCILIN gene (MYO) responsible for primary open angle glaucoma (GLCIA) Blochm. Biophys. Res. Commun. 242 (2), 396-400 (1998)			
JOURNAL MEDLINE REFERENCE	98113364 5 (bases 1 to 1228) Shimitzu,N. and Kudoh,J. Direct Submission Submitted (16-AUG-1997) to the DDBJ/EMBL/GenBank databases Nobuyoshi Shimitzu, Keio University School of Medicine, Department of Molecular Biology, 35 Shinanomachi, Shinjuku-Ku, Tokyo 160-8582			
JOURNAL TITLE				







SEQUENCE, 35 unordered pieces.  
AC023790  
VERSION AC023790.16 GI:9438256  
KEYWORDS HTG: HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota: Chordata: Craniata: Vertebrata: Euteleostomi;  
Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.  
1 (bases 1 to 193123)  
Muzny, D.M., Adams, C., Bailey, M., Barberia, J., Blankenburg, K.,  
Bodda, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C.,  
Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,  
David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N.,  
Dugan-Roches, S., Durbin, K.J., Fernandez, C., Ferraguto, D.,  
Forum-Tansey, J., Frantz, P., Ganesh, R., Gorrell, J.H., Gorrell, L.L.,  
Guerra, M., Harris, K., Hernandez, J., Hodgson, A., Hogue, M.,  
Hollway, C., Hosak, H., Jackson, L.E., Jackson, L., Jia, Y., Jones, M.,  
Kelly, S., Kondejewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z.,  
Lichtarge, O., Liu, J., Liu, W., Logan, O., Lozano, R.J., Lu, J.,  
Lucier, R., Martin, R., Martinez, C., McLeod, M.P., Mei, G., Morgan, M.,  
Morris, S., Nash, S., Nelson, A., Nguyen, R., Nguyen, N., Nguyen, S.,  
Oswal, G., Parish, B., Paxton, S., Payton, B., Perez, L., Pu, L.L.,  
Quiles, M., Reiter, D., Rives, M., Samuel, S., Say, J., Scherter, S.,  
Shah, E., Shen, H., Simon, M., Sparks, A., Stamps, A., Sugeng, R.,  
Taber, P., Taylor, T., Vasquez, L., Vinson, R., Vo, O., Wabnah, M.,  
Watlington, S., Weinstein, G., Weinstein, I.R., Williamson, A.,  
Worley, K., Wren, J., Wrensford, G., Yu, W., Zhou, X., Nelson, D. and  
Gibbs, R.  
Direct Submission  
Unpublished  
2 (bases 1 to 193123)  
Worley, K.C.  
Direct Submission  
Submitted (18-FEB-2000) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Jul 25, 2000 this sequence version replaced gi:9255941.  
----- Genome Center -----  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information -----  
Center project name: HABM  
Center clone name: RP11-377D9  
----- Summary Statistics -----  
Assembly program: PHRAP, version 0.990329  
Consensus quality: 167304 bases at least Q40  
Consensus quality: 176244 bases at least Q30  
Consensus quality: 181341 bases at least Q20  
Estimated insert size: 180060; sum-of-contrigs estimation  
Quality coverage: 0x in Q20 bases; agarose-IP estimation  
Quality coverage: 3.1x in Q20 bases; sum-of-contrigs estimation  
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\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank/draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 35 contrigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contrigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\*  
\* 1 21094: contrig of 21094 bp in length  
\* 21095 21194: gap of unknown length  
\* 21195 33930: contrig of 12736 bp in length  
\* 33931 34030: gap of unknown length  
\* 34031 48318: contrig of 14288 bp in length  
\* 48319 48418: gap of unknown length  
\* 48419 58799: contrig of 10381 bp in length  
\* 58800 58899: gap of unknown length  
\* 58900 68723: contrig of 9824 bp in length

\* 68724 68823: gap of unknown length  
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\* 75074 75174: gap of unknown length  
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\* 90047 90146: gap of unknown length  
\* 90147 90147: contrig of 5995 bp in length  
\* 95142 96241: gap of unknown length  
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\* 101874 101973: gap of unknown length  
\* 101974 108002: contrig of 6029 bp in length  
\* 108003 108102: gap of unknown length  
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\* 112904 113003: gap of unknown length  
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\* 126354 126453: gap of unknown length  
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\* 144632 144731: gap of unknown length  
\* 144732 150312: contrig of 5581 bp in length  
\* 150313 150412: gap of unknown length  
\* 150413 154114: contrig of 3702 bp in length  
\* 154115 154214: gap of unknown length  
\* 154215 158458: contrig of 4244 bp in length  
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\* 183205 184720: contrig of 1516 bp in length  
\* 184721 184820: gap of unknown length  
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\* 186238 188213: contrig of 1976 bp in length  
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1280 aggggtgagggtctgtgtcttacacctgtatgtcttacacctgagctcaatgcaacc 1339

b 54922 AGAGTCTGCTCTGTCATCCAGCTGGAGTGCAGTGGCAGATCTCAGCTCACTGCAACC 54863

1340 tctgcctccaggttcaagcaattctcctgtctcagcctcccgctagctggactacag 1399

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Db	54742	TGTGTCAGCGTGGTCTTTGAACCTCTGACCTCAGATGATCCACCTGCCTCCGCCA	54683
Qy	1512	gtgcgtggaattacagcattgatcatcacgcgcgcgcgcgcgaagtgctcaglttttaataagaa	1571
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Db	54622	CAATT 54618	

RESULT	11
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LOCUS	HUMYWXD03 136038 bp DNA PRI
DEFINITION	human sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
ACCESSION	E78810
VERSION	L78810.1 GI:1381111
KEYWORDS	
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE	1 (bases 1 to 135038)
AUTHORS	Chen,C.N., Su,Y., Baybayan,P., Siruno,A., Nagataj.R.,
TITLE	Mazzarella,R., Schlessinger,D. and Chen,E.
JOURNAL	Ordered shotgun sequencing of a 135 kb Xq25 YAC containing ANT2 and
MEDLINE	four possible genes, including three confirmed by EST matches
COMMENT	Nucleic Acids Res. 24 (20), 4034-4041 (1996)
	97078684
	Submitted by:

Advanced Center for Genetic Technology,  
Applied Biosystems Division of Perkin Elmer Corp., 850 Lincoln  
Center Drive,  
Foster City, CA 94404 USA  
and  
David Schlessinger,  
Department of Molecular Microbiology and Center for Genetics in  
Medicine  
Washington University School of Medicine,  
St. Louis MO 63110 USA  
e-mail: ellson@genseq.apdbio.com and david@genetics.wustl.edu  
Note: Gene predictions were accomplished with runs of Graftl  
versions 1.1 and 1.2, coupled with fasta and blastx comparisons to  
genbank & non-redundant peptide libraries. Repeat analysis was  
accomplished via a censor.  
The Rat EST105369 shows significant homology via blastx to this  
sequence  
Strand Start End  
top 9072 9326  
The Graves Disease carrier protein (X66035) shows significant  
homology via blastx to this sequence  
Strand Start End  
top 28802 29076  
top 35858 36081  
Comments for gene ANT-2 :  
This gene shows homology via blastx to the EST clone y115a12 Strand  
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repeat_region	5100, .5116 /note="LIkM repeat: matches 3151, .3167 of consensus"
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repeat_region	5765, .6075 /note="AluV repeat: matches 1, .311 of consensus"
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variation	
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Dz 57358 TCTGCTCCCAAGATTCAAAGTAACTCTCTGTGCTCTGCTCTGCGGTTGCTGGACTAAG 57299 	
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RESULT 13 ACO2639S/c HNG 15-JUN-2000 LOCUS Homo sapiens chromosome 10 clone RP11-45D20, WORKING DRAFT DEFINITION AC026395 ACCESSION AC026395 VERSION AC026395.3 GI:8567738 KEYWORDS HTGS_PHASEI; HTGS_DRAFT. SOURCE human. ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. REFERENCE Smith.D.R. (bases 1 to 152044) AUTHORS Smith.D.R. TITLE Genome Therapeutics Corporation Sequencing Center: Human Genome SEQUENCE DATA Unpublished JOURNAL 2 (bases 1 to 152044) REFERENCE Smith.D.R. AUTHORS Direct Submission JOURNAL Submitted (22-MAR-2000) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA COMMENT On Jun 15, 2000 this sequence version replaced gi:7330305.	
COMMENTS ----- Genome Center Center: Genome Therapeutics Corporation Center code: GTC Web site: http://www.genomecorp.com/ Contact: gtc-seqcenter@genomecorp.com	





DEFINITION Homo sapiens chromosome 10 clone RP11-78A18, WORKING  
DRAFT SEQUENCE, 26 unordered pieces.  
ACCESSION AC025947.3 GI:8439851  
VERSION AC025947.3  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 157057)  
AUTHORS Smith,D.R.  
TITLE Genome Therapeutics Corporation Sequencing Center: Human Genome  
Sequence Data  
JOURNAL Unpublished  
AUTHORS 2 (bases 1 to 157057)  
TITLE Smith,D.R.  
JOURNAL Direct Submission  
AUTHORS Submitted (18-MAR-2000) Genome Therapeutics Corporation, 100 Beaver  
JOURNAL Street, Waltham, MA 02453, USA  
COMMENT On Jun 10, 2000 this sequence version replaced gi:7528340.  
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Genome Center  
Center: Genome Therapeutics Corporation  
Center code: GTC  
Web site: http://www.genomecorp.com/  
Contact: gtc-seqcenter@genomecorp.com  
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Project Information  
Center project name: hg307  
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Summary Statistics  
Sequencing vector: N/A  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 990315  
Consensus quality: 140586 bases at least Q40  
Consensus quality: 148596 bases at least Q30  
Consensus quality: 150061 bases at least Q20  
Insert size: 154557; sum-of-ctrls  
Quality coverage: 3.7x in Q20 bases; sum-of-ctrls  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 26 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1 1544: contig of 1544 bp in length  
1545 1644: gap of unknown length  
1645 3218: contig of 1574 bp in length  
3219 3318: gap of unknown length  
3319 5022: contig of 1704 bp in length  
5023 5122: gap of unknown length  
5123 6553: contig of 1431 bp in length  
6554 6653: gap of unknown length  
6654 8651: contig of 1998 bp in length  
8652 8751: gap of unknown length  
8752 10843: contig of 2092 bp in length  
10844 10943: gap of unknown length  
10944 13772: contig of 2829 bp in length  
13773 13872: gap of unknown length  
13873 15825: contig of 1953 bp in length  
15826 15925: gap of unknown length  
15926 19591: contig of 3666 bp in length  
19592 19691: gap of unknown length  
19692 22350: contig of 2659 bp in length  
22351 22450: gap of unknown length  
22451 25948: contig of 3498 bp in length  
25949 26048: gap of unknown length  
26049 29741: contig of 3593 bp in length  
29742 29742: gap of unknown length  
29743 34105: contig of 4364 bp in length  
34106 34205: gap of unknown length  
34206 38484: contig of 4279 bp in length  
38485 38584: gap of unknown length

38585 41992: contig of 3408 bp in length  
41993 42092: gap of unknown length  
42093 42920: contig of 5828 bp in length  
42921 48020: gap of unknown length  
48021 47921: gap of unknown length  
48022 54416: contig of 6396 bp in length  
54417 54516: gap of unknown length  
54517 60194: contig of 5678 bp in length  
60195 60294: gap of unknown length  
60295 67639: contig of 7345 bp in length  
67640 67739: gap of unknown length  
67740 74790: contig of 7051 bp in length  
74791 74890: gap of unknown length  
74891 85632: contig of 10741 bp in length  
85632 85731: gap of unknown length  
85732 93940: contig of 8209 bp in length  
93941 94040: gap of unknown length  
94041 104191: contig of 10151 bp in length  
104192 104291: gap of unknown length  
104292 116387: contig of 12096 bp in length  
116388 116487: gap of unknown length  
116488 135857: contig of 19370 bp in length  
135858 135957: gap of unknown length  
135958 157057: contig of 21100 bp in length.  
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1. 157057  
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/db\_xref="taxon:9606"  
/chromosome="Chromosome 10"  
/clone="RP11-78A18"  
/clone\_1b="RPCT-11"  
BASE COUNT 45178 a 32550 c 32372 g 44448 t 2509 others  
ORIGIN  
Query Match 3.5% Score 185.8; DB: 78; Length 157057;  
Best Local Similarity 80.8%; Pred. No. 7.1e-30;  
Matches 232; Conservative 0; Mismatches 47; Indels 8; Gaps 1;  
Oy 1321 accatgactcctcaactcctcctccaggctcaagcaactcctcgtcagccctc 1380  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 109551 ATCTGGCTCTCACTGCACTCACCCTCCCGGTTCACTGATTTCTCGCTCAGCCCTCC 109492  
Oy 1381 cgcgtagctgggaactacagc-----gcacgcgcgcgcgaatttctgtatctga 1432  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 109491 TGAGTAGCTGGGATTACAGCACCACTACCAAGCCGACGCAATTTTGTATTTA 109432  
Oy 1433 gagatgggttccacacattatgaagccggctgtcttggaacccctgactcagtgatcca 1492  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 109431 GAGATGGGCTTCCACCAATGTGGCCAGCGCTGTGAACCTCGACCTCAGGTGATCCA 109372  
Oy 1493 cccacctagcctctcaagtgctggggttacaggaatgagcagccgcgcgcgaagg 1552  
||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 109371 CCCGCTTAGCTCCCAAGGCTGGGATTACAGGATGACCCACTGCACCTGGCCAA 109312  
Oy 1553 gtccagtgcttaaggaataacttgaaatgttacttaaccacacag 1599  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 109311 TTAATTTTAAATGAATAATGATGATTTTAAAAAACAACAG 109265  
RESULT 15  
AC015488 161499 bp DNA HTG 16-MAR-2000  
LOCUS AC015488  
DEFINITION Homo sapiens clone RP11-20F6, WORKING DRAFT SEQUENCE, 16 unordered  
pieces.  
ACCESSION AC015488  
VERSION AC015488.4 GI:7107977  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 161499)  
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.

TITLE Homo sapiens, clone RP11-20F6  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 161499)  
AUTHORS Bairren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,  
Baldwin,J., Barna,N., Beckery,R., Boguslavsky,L., Boukhalter,B.,  
Brown,A., Castle,E., Colangelo,M., Collins,S., Collamore,A.,  
Cooke,P., Dearellano,K., Dewar,K., Domingo,M., Donelan,L., Doyle,M.,  
Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,  
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Harford,A., Horton,L.,  
Howland,J.C., Johnson,R., Jones,C., Kamp,L., Karas,A., Klein,J.,  
Lehocky,J., Lien,C., Locke,K., Macdonald,P., Marquis,N.,  
Mcwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,  
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,  
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,  
Stange-Thomann,N., Stojanovic,N., Sudramanlan,A., Talamas,J.,  
Testa,E.S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,  
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (16-NOV-1999) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Feb 28, 2000 this sequence version replaced gi:6715933.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
-----  
Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: MIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence.submissions@genome.wi.mit.edu](mailto:sequence.submissions@genome.wi.mit.edu)  
-----  
Project Information  
-----  
Center project name: L2895  
Center clone name: 20\_F\_6  
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Summary Statistics  
Sequencing vector: M13; M77815: 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 152793 bases at least Q40  
Consensus quality: 156653 bases at least Q20  
Consensus quality: 158136 bases at least Q20  
Insert size: 160000; agarose-ff  
Insert size: 159999; sum-of-contigs  
Quality coverage: 5.9 in Q20 bases; agarose-ff  
Quality coverage: 5.9 in Q20 bases; sum-of-contigs  
-----  
NOTE: This is a 'working draft' sequence. It currently  
consists of 16 contigs. The true order of the pieces  
is not known and their order in this sequence record is  
arbitrary. Gaps between the contigs are represented as  
runs of N, but the exact sizes of the gaps are unknown.  
This record will be updated with the finished sequence  
as soon as it is available and the accession number will  
be preserved.  
-----  
1 2206: contig of 2206 bp in length  
\* 2207 2306: gap of 100 bp  
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\* 6911 7010: gap of 100 bp  
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\* 9819 9918: gap of 100 bp  
\* 9919 13394: contig of 3476 bp in length  
\* 13395 13494: gap of 100 bp  
\* 13495 17122: contig of 3628 bp in length  
\* 17123 17222: gap of 100 bp  
\* 17223 19752: contig of 2530 bp in length  
\* 19753 19852: gap of 100 bp  
\* 19853 23958: contig of 4106 bp in length  
\* 23959 24058: gap of 100 bp  
\* 24059 29684: contig of 5626 bp in length  
\* 29685 29784: gap of 100 bp  
\* 29785 33951: contig of 4167 bp in length  
\* 33952 34051: gap of 100 bp  
\* 34052 39841: contig of 5790 bp in length  
\* 39842 39941: gap of 100 bp  
\* 39942 48297: contig of 8356 bp in length

QY	1463	ggtctgaactccctgaactcagtgatcatcaccacctaagctcctctaagtgctggatt	1522
QY	1463	ggtctgaactccctgaactcagtgatcatcaccacctaagctcctctaagtgctggatt	1522
DB	16889	CATGCCAGGCTAATTTTGTGTTTAGTGAAGATAGGGGTTTGCCATGTGGCCAGCCT	16948
QY	1403	cagccgcggctaatcttctgtatctgtatagtagagatgggggttcacacatatagccggct	1462
DB	16829	GCCTCCAGATTCAAGCAATTCTCTGCTCAGCCTCTCGAATACCTGGGTTATAGCA	16888
QY	1343	gctcccaaggtccaagcaattctcctgtctcagcctcccgtagctggactacagcg	1402
DB	16769	gTCTGCTGTGTCACCCAGCGGAGGCGAGTGCAACCTCTGCGCTCACTGCACACTCT	16828
QY	1283	gtgagaggtctgtgtcttaactactactcgtatgctctacacccgtgagctactgcaactct	1342
DB	16769	gTCTGCTGTGTCACCCAGCGGAGGCGAGTGCAACCTCTGCGCTCACTGCACACTCT	16828
QY	1403	cagccgcggctaatcttctgtatctgtatagtagagatgggggttcacacatatagccggct	1462
DB	16889	CATGCCAGGCTAATTTTGTGTTTAGTGAAGATAGGGGTTTGCCATGTGGCCAGCCT	16948
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